I claim:

1. A method for transcript analysis, comprising:

a. providing multiple polynucleotides derived from a multiplicity of mRNAs derived from a biological sample, said polynucleotides having homology to at least one known reference sequence;

b. expressing said polynucleotides; and

c. assessing at least one physical property of the expression products obtained thereby to determine the sequences of said polynucleotides by comparing said at least one physical property to the predicted properties of polypeptides encoded in said known reference sequence.

2. A method for genetic analysis, comprising:

a. providing multiple polynucleotides derived from a multiplicity of mRNAs derived from a biological sample, said polynucleotides having homology to at least one known reference sequence;

b. expressing said polynucleotides; and

c. assessing at least one physical property of the expression products obtained thereby to determine the sequences of said polynucleotides by comparing said at least one physical property to the predicted properties of polypeptides encoded in said known reference sequence.

3. A method for genetic analysis, comprising:

a. providing two or more nucleic acid samples derived from two or more biological samples, said biological samples being heterogenous and further containing multiple polynucleotides derived from a multiplicity of mRNAs derived from a biological sample;

b. expressing said polypeptides from said polynucleotides;

c. subjecting said polypeptides, in combination, to physical property assessment; and

d. comparing the results of said physical property assessment to predicted properties of polypeptides encoded in at least one reference sequence.

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4. Providing a nucleic acid molecule;

expressing polypeptides from two or more reading frames of said nucleic acid sample; and

determining the masses of said polypeptides to create a peptide mass signature characteristic of said nucleic acid molecule.